

Amendments to the Specification:

Please amend the paragraph beginning at page 46, line 24, as follows.

Figs. 39A and 39B illustrate that *daf-18* encodes a homologue of PTEN (MMAC/TEP1). Fig. 39A shows the exon/intron structure of DAF-18 (SEQ ID NOS:306, 307, 327, and 328). The phosphatase domain is indicated in gray. The bottom of this figure indicates that *daf-18(e1375)* has a 30 base pair insertion in the fourth exon. 13 base pairs (shaded) are duplicated along with two smaller segments of the repeat (thick bars). This mutation introduces a premature stop codon (*). Fig. 39B shows an alignment of the phosphatase domains of DAF-18 and PTEN (GeneBank accession U93051) (SEQ ID NOS:308 and 309). Pileup (GCG) was used to align the entire coding sequence. The phosphatase domain is shown with identical amino acids shaded. The probable active site Cys-(X)₅-Arg sequence is indicated with a bar.

Please amend the paragraph beginning at page 83, line 14 as follows:

Score = 151 (68.4 bits), Expect = 1.9e-140, Sum P(8) = 1.9e-140

Identities = 28/54 (51%), Positives = 38/54 (70%)

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AFX: 226 SPVGHFAKWGSPCSRNRREEADMWTTFRPRSSSNASSVSTRLSPLRPESEVLAE 279
                                           (SEQ ID NO:161)
      SP   F+KW   SP S + ++ D W+TFRPR+SSNAS++S RLSP+   E + L E
                                           (SEQ ID NO:162)
FKHR: 287 SPGSQFSKWPASPGSHSNDDFDNWSTF██████████ NASTISGRLSPIMTEQDDLGE 340
                                           (SEQ ID NO:163)
DAF-16a                SFRPRTQSNLSIPGSSS        (SEQ ID NO:164)
                        ██████████
                        ██████████
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Score = 132 (59.8 bits), Expect = 1.9e-140, Sum P(8) = 1.9e-140

Identities = 22/42 (52%), Positives = 28/42 (66%)

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AFX:      7 KAAAIIDLPDFEPQSRPRSCWTWPLPRPEIANQPSEPPEVEP 48 (SEQ ID NO:165)
          +A ++++DPDFEP RPRSCWTWPLPRPE + S P (SEQ ID NO:166)
FKHR:      3 EAPQVVEIDPDFEPLRPRSCWTWPLPRPEFSQSNSATSSPAP 44 (SEQ ID NO:167)
DAF-16    TFMNTPDDVMMNDDMEPIPRDRCNTWPMRRPQLEPPLNSSP 177 (SEQ ID NO:168)
          T ++P+ V ++ D EP+PR R TWP+ RP++ + ++++ (SEQ ID NO:169)

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Please amend the paragraph beginning at page 96, line 15, as follows.

From the same genetic screen that generated the *akt-1(mg144gf)* allele, we identified another *age-1* suppressor, *mg142*. This mutation also bypasses the need for upstream *age-1* signaling and is genetically dominant. Genetic mapping placed the mutation in the region where a *C. elegans* homologue maps. The genomic sequence of *pdk-1*, starting 60 bp upstream of the start codon and ending 60 bp downstream of the stop codon is shown in Figure 35 (SEQ ID NO: 158). Figures 36 and 37 show the two *C. elegans pdk-1* spliced forms, *pdk-1a* (Figure 36; SEQ ID NO: 159) and *pdk-1b* (Figure 37; SEQ ID NO: 160). The *pdk-1(mg142)* gain of function mutation is Ala303Val (splice 1). This protein is 58% identical to mammalian PDK in the pleckstrin homology domain and 39% identical in the kinase domain as shown below (SEQ ID NOS:~~170-201~~ 170-202).

Please amend the paragraph beginning at page 97, line 2, as follows:

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Score = 252 (88.7 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 47/80 (58%), Positives = 60/80 (75%), Frame = +3

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Query:      439 LEKQAGGNPWHQFVENNLILKMGPVDKRKGLFARRRQLLLTEGPHLYYVDPVNKVLKGEI 498
          LE+Q NP+H F N+LILK G ++K++GLFARRR LLTEGPHL Y+D N VLKGE+
Sbjct:     1818 LEEQRVKNPFHIFTNNSLILKQGYLEKKRGLFARRRMFLLTEGPHLLYIDVPNLVLKGEV 1997

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Query: 499 PWSQELRPEAKNFKTFFVHT 518 (SEQ ID NO:170)
PW+ ++ E KN TFF+HT (SEQ ID NO:171)
Sbjct: 1998 PWTPCMQVELKNSGTFFIHT 2057 (SEQ ID NO:172)

Score = 201 (70.8 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 48/123 (39%), Positives = 72/123 (58%), Frame = +1

Query: 263 SDLWALGCIYQLVAGLPPFRAGNEYLIQKIIKLEYDFPEKFFPKARDLVEKLLVLDAT 322
+D+W LGCI++Q +AG PPFRA N+Y + ++I +L++ FPE F +A +++ K+LV
Sbjct: 802 TDIWGLGCILFQCLAGQPPFRAVNQYHLLKRIQELDFSPEGFPEEASEIIAKILV-G*H 978

Query: 323 KRLGCE----EMEGYGP-----LKAHPFFESVTWENLHQQTTPPKLTAYLPAMSEDDE 370
+ L E ++ P L AH FFE+V W N+ PP L AY+PA + E
Sbjct: 979 ETLKTEYVIFNLQVRDPSTRITSQELMAHKFFENVVDWVNIANIKPPVLHAYIPATFGEPE 1158

Query: 371 DCYGN 375 (SEQ ID NO:173)
Y N (SEQ ID NO:174)
Sbjct: 1159 -YYSN 1170 (SEQ ID NO:175)

Score = 180 (63.4 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 31/72 (43%), Positives = 52/72 (72%), Frame = +2

Query: 157 FGLSYAKNGELLKYIRKIGSFDETCTRFYTAEIVSALEYLHGKGIHRDLKPENILLNED 216
F + +NG+L + + GSFD ++F+ +EI++ L++LH I+HRD+KP+N+L+ +D
Sbjct: 287 FVIGLVENGDLGESLCHFGSFDMLTSKFFASEILTGLQFLHDNKIVHRDMKPDNVLIQKD 466

Query: 217 MHIQITDFGTAK 228 (SEQ ID NO:176)
HI ITDFG+A+ (SEQ ID NO:177)
Sbjct: 467 GHILITDFGSAQ 502 (SEQ ID NO:178)

Score = 83 (29.2 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 15/53 (28%), Positives = 32/53 (60%), Frame = +2

Query: 108 YAIKILEKRHIKENKVPYVTRERDVMSRLD-----HPFFVKLYFTFQDDEKL 155
+ A+K+L+K ++ + K+ + RE+++++ L HPF +LY F D ++ (SEQ ID NO:179)
Sbjct: 8 FAVKVLQKSYLNRHQKMDAIIREKNILTYLSQECGGHPFVTQLYTHFHDQARI 166 (SEQ ID NO:180)
(SEQ ID NO:181)

Score = 81 (28.5 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 15/29 (51%), Positives = 19/29 (65%), Frame = +2

Query: 519 PNRYYLMDPSGNAHKWCRKIQEVWRQRY 547 (SEQ ID NO:182)
PNR YYL D A +WC+ I +V R+RY (SEQ ID NO:183)
Sbjct: 2129 PNRVYYLFDLEKKADEWCKAINDV-RKRY 2212 (SEQ ID NO:184)

Score = 78 (27.5 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 15/25 (60%), Positives = 18/25 (72%), Frame = +3

Query: 232 PESKQARANSFVGTAQYVSPPELLTE 256 (SEQ ID NO:185)
PE AR +FVGTA YVSPE+L + (SEQ ID NO:186)
Sbjct: 660 PEENTARRTTFVGTAQYVSPPEMLAD 734 (SEQ ID NO:187)

Please amend the paragraph beginning at page 98, line 3, as follows:

Overall, *C. elegans pdk-1* exhibits the following homology to human PDK-1.

Score = 118 (54.4 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 21/62 (33%), Positives = 41/62 (66%)

Query: 63 KRTSNDFMFLQSMGEGAYSQVFRCREVATDAMFAVKVLQKSYLNRHQKMDAIIREKNILT 122
K+ DF F + +GEG++S V RE+AT +A+K+L+K ++ + K+ + RE+++++
Sbjct: 76 KKRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIIKENKVPYVTRERDVMS 135

Query: 123 YL 124 (SEQ ID NO:188)
L (SEQ ID NO:189)
Sbjct: 136 RL 137 (SEQ ID NO:190)

Score = 230 (106.0 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 39/90 (43%), Positives = 63/90 (70%)

Query: 131 HPFVTQLYTHFHDQARIYFVIGLVENGDLGESLCHFGSFDMLTSKFFASEILTGLQFLHD 190
HPF +LY F D ++YF + +NG+L + + GSFD ++F+ +EI++ L++LH
Sbjct: 139 HPFFVKLYFTFQDDEKLYFGLSYAKNGELLKYIRKIGSFDETCTRFYTAEIVSALEYLHG 198

Query: 191 NKIVHRDMKPDNVLIQKDGHILITDFGSAQ 220 (SEQ ID NO:191)
I+HRD+KP+N+L+ +D HI ITDFG+A+ (SEQ ID NO:192)
Sbjct: 199 KGIIHRDLKPENILLNEDMHIQITDFGTAK 228 (SEQ ID NO:193)

Score = 238 (109.7 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 43/98 (43%), Positives = 67/98 (68%)

Query: 259 EENTARRTTFVGTA LYVSPEMLADGDVGPQTDIWGLGCILFQCLAGQPPFRAVNQYHLLK 318
E AR +FVGTA YVSPE+L + +D+W LGCI++Q +AG PPFA N+Y + +
Sbjct: 233 ESKQARANSFVGTAQYVSPELLTEKSACKSSDLWALGCIIYQLVAGLPPFRAGNEYLIHQ 292

Query: 319 RIQELDFSFPGEFPPEEASEIIAKILVRDPSTRITSQEL 356 (SEQ ID NO:194)
+I +L++ FPE F +A +++ K+LV D + R+ +E+ (SEQ ID NO:195)
Sbjct: 293 KIIKLEYDFPEKFFPKARDLVEKLLVLDTAKRLGCEEM 330 (SEQ ID NO:196)

Score = 85 (39.2 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 17/35 (48%), Positives = 21/35 (60%)

Query: 356 LMAHKFFENVVDWVNIANIKPPVLHAYIPATFGEPE 390 (SEQ ID NO:197)
L AH FFE+V W N+ PP L AY+PA + E (SEQ ID NO:198)
Sbjct: 336 LKAHPFFESVTWENLHQQTTPPKLTAYLPAMSEDDE 370 (SEQ ID NO:199)

Score = 324 (149.3 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 59/104 (56%), Positives = 75/104 (72%)

Query: 458 LEEQVRKNPFFHIFTNNSLILKQGYLEKKRGLFARRRMFLLTEGPHLLYIDVPNLVLKGEV 517
LE+Q NP+H F N+LILK G ++K++GLFARRR LLTEGPHL Y+D N VLKGE+
Sbjct: 439 LEKQAGGNPWHQFVENNLILKMGPVDKRGKGLFARRRQLLLTEGPHLYYVDPVNKVLKGEI 498

Query: 518 PWTPCMQVELKNSGTFFIHTPNRVYYLFDLEKKADEWCKAINDV 561 (SEQ ID NO:200)
PW+ ++ E KN TFF+HTPNR YYL D A +WC+ I +V (SEQ ID NO:201)
Sbjct: 499 PWSQELRPEAKNFKTFFVHTPNRTYYLMDPSGNAHKWCRKIQEV 542 (SEQ ID NO:202)

Please amend the paragraph beginning at page 99, line 12, as follows.

Mapping of the *mg142* mutation to this open reading frame establishes the function of this protein. It is much more closely related to PDK than to any other known kinase. PDK is a mammalian kinase that phosphorylates an essential serine residue on AKT, contributing to its activation. The region of *akt-1* phosphorylated by PDK-1 is shown below (~~SEQ ID NO: 202-207~~ SEQ ID NOS:203-207 and 305).

Please amend the paragraph beginning at page 99, line 18, as follows:

human AKT 276 KLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEV 320 (SEQ ID NO:203)
KLENL+LDKDGHIKI DFGLCKE I G TFCGTPEYLAPEV (SEQ ID NO:204)
Ce akt-133509 KLENLLLDKDGHIKIADFGLCKEEISFGDKTSTFCGTPEYLAPEV 33643 (SEQ ID NO:205)
Ceakt2 326 LCKEEIKYGDKTSTFCGTPEYLAPEVIEDIDYDRSVDWWGVGVVMMYEMMCGRLPFSKENGK
(LCKE I G TFCGTPEYLAPEV+ED DYR+VDWWG+GVVMMYEMMCGRLPF +++ + (SEQ ID NO:206)
(LCKE I G TFCGTPEYLAPEV+ED DYR+VDWWG+GVVMMYEMMCGRLPF +++ + (SEQ ID NO:207)
moAKT: 298 LCKEGISDGATMKTFCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMMYEMMCGRLPFYNQDHER
(LCKE I G TFCGTPEYLAPEV+ED DYR+VDWWG+GVVMMYEMMCGRLPF +++ + (SEQ ID NO:305)

Please amend the paragraph beginning at page 178, line 3, as follows:

Pepck

>R11A5

Length = 26,671

Plus Strand HSPs:

Score = 994 (461.5 bits), Expect = 0.0, Sum P(5) = 0.0

Identities = 176/223 (78%), Positives = 195/223 (87%), Frame = +1

Query: 201 AKNNGEFVRCVHSVGPQPKPVATKVINHWPCNPEKTIIAHRPAEREIWSFGSGYGGNSLLG 260

A N +FVRC+HSVG P+PV +VINHWPCNPE+ +IAHRP EREIWSFGSGYGGNSLLG

Sbjct: 8682 ALGNQDFVRCIHSVGLPRPVKQRVINHWPCNPERVLIAHRPPEREIWSFGSGYGGNSLLG 18861

Query: 261 KKCFAIRIAMNIGYDEGWMAEHMLIMGVTSPKGEERFVAAAFPSACGKTNLAMLEPTIPG 320

KKCFALRIA NI DEGWMMAEHMLIMGVT P G E F+AAAFPSACGKTNLAMLEPT+PG

Sbjct: 18862 KKCFAIRIASNIAKDEGWMAEHMLIMGVTRPCGREHFIAAFPSACGKTNLAMLEPTLPG 19041

Query: 321 WKVRVIGDDIAWMKFGADGRLYAINPEYGFVGAPGTSKTNPMAMASFQENTIFTNVAE 380

WKVR +GDDIAWMKFG DGRLYAINPE GFFGVAPGTS+KTNPMA+A+FQ+N+IFTNVAE

Sbjct: 19042 WKVRCVGGDDIAWMKFGEDGRLYAINPEAGFFGVAPGTSNKNPMMAVATFQKNSIFTNVAE 19221

Query: 381 TADGEYFWEGLEHEVKNPKVDMINWLGEPCWHIGDESKAAHPNS 423 (SEQ ID NO:211)

TA+GEYFWEGLE E+ + VD+ WLGE WHIG+ AAHPNS (SEQ ID NO:212)

Sbjct: 19222 TADGEYFWEGLEDEIADKNVDITTLWLGKWHIGEPGVAAHPNS 19350 (SEQ ID NO:213)

Score = 657 (305.1 bits), Expect = 0.0, Sum P(5) = 0.0

Identities = 120/173 (69%), Positives = 144/173 (83%), Frame = +1

Query: 32 KGDFVSLPKHVQRFVAEKAELMKPSAIFICDGSQNEADELIARCVRGVLVPLKAYKNNY 91

+GDF LP VQRF+AEKAELM+P IFICDGSQ+EADELI + +ERG+L L+AY+NNY

Sbjct: 18181 QGDFHLLPAKVQRFIAEKAELMRPRGIFICDGSQNEADELIDKLIERGMLSKLEAYENNY 18360

Query: 92 LCRTDPRDVARVESKTWMITPEKYDSVCHTPEGVKPMGQWMSPEFGKELDDRFPGCMA 151

+CRTDP+DVARVESKTWM+T KYD+V HT EGV+P+MG W++P++ ELD RFPGCMA

Sbjct: 18361 ICRTDPKDVARVESKTWMVTKNKYDTVTHTKEGVEPIMGHWLAPEDLATELDSRFPGCMA 18540

Query: 152 GRTMYVIPYSMGPVGGPLSKIGIELTDSYVVLICMRIMTRMGEPVLKALAKNN 204

(SEQ ID NO:214)

GR MYVIP+SMGPVGGPLSKIGI+LTDS+YVVL MRIMTR+ V AL +

(SEQ ID NO:215)

Sbjct: 18541 GRIMYVIPFSMGPVGGPLSKIGIQLTDSNYVVLICMRIMTRVNDVWDALGNQD 18699

(SEQ ID NO:216)

Score = 453 (210.3 bits), Expect = 0.0, Sum P(5) = 0.0
Identities = 77/107 (71%), Positives = 90/107 (84%), Frame = +1

Query: 424 RFTAPAGQCPIIHPDWEKPEGVPIDAIIFGGRRPEGVPLVFESRSWVHGIFVGACVKSEA 483
RF APA QCPIIHPDWE P+GVPI+AIIFGGRRP+GVPL++E+ SW HG+F G+C+KSEA
Sbjct: 19396 RFAAPANQCPIIHPDWESPQGVPIEAIIFGGRRPQGVPLIYETNSWEHGVFTGSCLKSEA 19575

Query: 484 TAAAEHTGKQVMHDPAMRPFMGYNFGRYMRHWMKLGQPPHKVPKIF 530 (SEQ ID NO:217)
TAAAE TKG VMHDPAMRPFMGYNFG+Y++HW+ L KV F (SEQ ID NO:218)
Sbjct: 19576 TAAAEFTGKTVMHDPAMRPFMGYNFGKYLQHWLDLKTDSRKVIDFF 19716 (SEQ ID NO:219)

Score = 404 (187.6 bits), Expect = 0.0, Sum P(5) = 0.0
Identities = 68/116 (58%), Positives = 89/116 (76%), Frame = +1

Query: 526 VPKIFHVNWFRQSADHKFLWPGYGDNIRVIDWILRRCSGDATIAEETPIGFIPKKGTINL 585
+PKI+HVNWFR+ +++KFLWPG+GDNIRVIDWI+RR G+ I ETPIG +P KG+INL
Sbjct: 19750 MPKIYHVNWFRKDSNNKFLWPGFGDNIRVIDWIIRRLDGEQEIGVETPIGTVPKGSINL 19929

Query: 586 EGLPNVNWDELMSIPKSYWLEDVETKTFFENQVGS DLPPEIAKELEAQTERIKAL 641
(SEQ ID NO:220)
EGL VNWDELMS+P YW +D E + F + QVG DLP + E++AQ +R++ L (SEQ ID NO:221)
Sbjct: 19930 EGLGEVNWDELMSVPADYWKQDAQEIRKFLDEQVGEDLPEPVRAEMDAQEKRVQTL 20097
(SEQ ID NO:222)

Score = 69 (32.0 bits), Expect = 0.0, Sum P(5) = 0.0
Identities = 15/36 (41%), Positives = 21/36 (58%), Frame = +1

Query: 5 SLSHFKDDDDFAVVSEVVTHKQNHIPVIKGFVSLPK 40 (SEQ ID NO:223)
SL +D F VV+EVV + H+P++K F S K (SEQ ID NO:224)
Sbjct: 14722 SLRQISED AFYVVNEVVMKRLGHVPILKVIFESSEK 14829 (SEQ ID NO:225)

Score = 39 (18.1 bits), Expect = 6.9e-244, Sum P(4) = 6.9e-244
Identities = 9/25 (36%), Positives = 11/25 (44%), Frame = +3

Query: 148 GCMAGRTMYVIPYSMGPVGGPLSKI 172 (SEQ ID NO:226)
GC R + V P S PL K+ (SEQ ID NO:227)
Sbjct: 8040 GCSGRRVLCVCPCSHSSSALPLQKV 8114 (SEQ ID NO:228)

Score = 38 (17.6 bits), Expect = 4.0e-285, Sum P(5) = 4.0e-285
Identities = 7/16 (43%), Positives = 9/16 (56%), Frame = +1

Query: 588 LPNVNWDELMSIPKSY 603 (SEQ ID NO:229)
L + NW +S P SY (SEQ ID NO:230)
Sbjct: 22654 LESFNWFSFVSCPDSY 22701 (SEQ ID NO:231)

Score = 37 (17.2 bits), Expect = 2.0e-48, Sum P(3) = 2.0e-48
Identities = 6/14 (42%), Positives = 9/14 (64%), Frame = +1

Query: 117 SVCHTPEGVKPMMG 130 (SEQ ID NO:232)
+V H P ++P MG (SEQ ID NO:233)
Sbjct: 19603 TVMHDPMAMRPFMG 19644 (SEQ ID NO:234)

Please amend the paragraph beginning at page 180, line 9, as follows:

Acetyl coa carboxylase

>W09B6

Length = 32,900
Plus Strand HSPs:

Score = 562 (259.1 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 109/197 (55%), Positives = 138/197 (70%), Frame = +2

Query: 1951 SGFFDYGSFSEIMQPWAQTVVVGRARLGGIPVGVVAVETRTVELSVPADPANLDSEAKII 2010
+G D SF EI WA+++V GRARL GIP+GVV+ E R VPADPA S+ +
Sbjct: 28280 TGICDTMSFDEICGDWAKSIVAGRARLCGIPIGVVSSEFRNFSTIVPADPAIDGSQVQNT 28459

Query: 2011 QQAGQVWFPSAFKTYQAIKDFNREGLPLMVFANWRGFSGGMKDMYDQVLKFGAYIVDGL 2070
Q+AGQVW+PDSAFKT +AI D N+E LPLM+ A+ RGFSGG KDMYD VLKFGA IVD L
Sbjct: 28460 QRAGQVWYPDSAFKTAEAINDLNKENLPLMIIASLRGFSGGQKDMYDMVLKFGAQIVDAL 28639

Query: 2071 RECSQPVMVYIPPAELRGGSWVIDPTINPRHMEMYADRESRGSVLEPEGTVEIKFRKK 2130
++PV+VYIP ELRGG+W V+D I P + + AD +SRG +LEP V IKFRK
Sbjct: 28640 AVYNRPVIVYIPEAGELRGGAWAVLDSKIRPEFIHLVADEKSRGGILEPNAVVGKFRKP 28819

Query: 2131 DLVKTMRRVDPVYIRLA 2147 (SEQ ID NO:235)
+++ M+R DP Y +L+ (SEQ ID NO:236)
Sbjct: 28820 MMMEMMKRSDPTYSKLS 28870 (SEQ ID NO:237)

Score = 357 (164.6 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 68/124 (54%), Positives = 89/124 (71%), Frame = +2

Query: 303 VGYPVMIKASEGGGGKGIRKVNADDFFPNLFRQVQAEVPGSPIFVMRLAKQSRHLEVQIL 362
+G+P+MIKASEGGGGKGIRK +DF ++F +V EV GSPIF+M+ +RH+EVQ+L
Sbjct: 23264 IGFPLMIKASEGGGGKGIRKCTKVEDFKSMFEEVAQEVQGSPIFLMKCVDGARHIEVQLL 23443

Query: 363 ADQYGN AISLFGRDCSVQRRHQKXXXXXXXXXXXXXVFEHMEQCAVKLAKMVGYSAGTV 422
AD+Y N IS++ RDCS+QRR QK + + M++ AV+LAK VGY SAGTV
Sbjct: 23444 ADRYENVISVYTRDCSIQRRQKIIEEAPAI IASSHIRKSMQEDAVRLAKYVGYESAGTV 23623

Query: 423 EYLY 426 (SEQ ID NO:238)
EYLY (SEQ ID NO:239)
Sbjct: 23624 EYLY 23635 (SEQ ID NO:240)

Score = 345 (159.1 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 65/116 (56%), Positives = 86/116 (74%), Frame = +2

Query: 1787 KEEGLGAENLRGSGMIAGESSLAYDEIITISLVT CRAIGIGAYLVRLGQRTIQVENS HLI 1846
K E +G ENL+GSG+IAGE++ AY E+ T VT R++GIGAY RL R +Q + SHLI
Sbjct: 27794 KNEKIGVENLQGSGLIAGETARAYAEVPTYCYVTGRSVGIGAYTARLAHRIVQHKQSHLI 27973

Query: 1847 LTGAGALNKVLGREVYTSNNQLGGIQIMHNNGVTHCTVCDDFEGVFTVLHWLSYMP 1902
(SEQ ID NO:241)
LTG ALN +LG++VYTSNNQLGG ++M NGVTH V +D EG+ V+ W+S++P (SEQ ID NO:242)
Sbjct: 27974 LTGYEALNTLLGKKVYTSNNQLGGPEVMFRNGVTHAVVDNDLEGI AKVIRWMSFLP 28141
(SEQ ID NO:243)

Score = 319 (147.1 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 59/119 (49%), Positives = 80/119 (67%), Frame = +2

Query: 503 HVIAARITSENPDEGFKPSSGTVQELNFRSNKNVWGYFSVAAAGGLHEFADSQFGHCFSW 562
H IAARIT ENPD+ F+PS+G V E+NF S+++ W YFSV +H+FADSQFGH F+
Sbjct: 23870 HAIAARITCENPDDSRPSTGKVYEINFPSSQDAWAYFSVGRGSSVHQFADSQFGHIFTR 24049

Query: 563 GENREEAISNMVVALKELSIRGDFRTTVEYLIK LLETESFQLNRIDTGWLDRLIAEKVQ 621
(SEQ ID NO:244)
G +R EA++ M LK ++IR F T V YL+ L+ F N +T WLD+ IA K++
(SEQ ID NO:245)
Sbjct: 24050 GTSRTEAMNTMCSTLKHMTIRSSFPTQVNYLV DLMHDADFINNAFNTQWLDKRIAMKIK 24226
(SEQ ID NO:246)

Score = 303 (139.7 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 55/90 (61%), Positives = 70/90 (77%), Frame = +2

Query: 178 PGGANNNNYANVELILDIAKRIPVQAVWAGWGHASENP KLPELLKNGIAFMGPPSQAMW 237
P G N NN+ANV+ IL A + V AVWAGWGHASENP LP L + IAF+GPP+ AM+
Sbjct: 22886 PSGTNKNNFANVDEILKHAIKYEVD AVWAGWGHASENPDLPRRLNDHNI AFIGPPASAMF 23065

Query: 238 ALGDKIASSIVAQTAGIPTLPWSGSGLRVD 267 (SEQ ID NO:247)
+LGDKIAS+I+AQT G+PT+ WSGSG+ ++ (SEQ ID NO:248)
Sbjct: 23066 SLGDKIASTIIAQTGVVPTVAWSGSGITME 23155 (SEQ ID NO:249)

Please amend the paragraph beginning at page 182, line 3, as follows:

Trehelase

>C23H3

Length = 39,721

Minus Strand HSPs:

Score = 227 (104.5 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95

Identities = 36/67 (53%), Positives = 51/67 (76%), Frame = -2

Query: 2 VIKNLGYMVDNHGFVPNGGRVYYLTRSQPPLLTPMVYEYYMSTGDLDFVMEILPTLDKEY 61
+I N +++++ GFVPNGGRVYYL RSQPP PMVYEYY++T D+ V +++P ++KEY
Sbjct: 9798 MILNFAHIIETYGFVPNGGRVYYLRRSQPPFFAPMVYEYYLATQDIQLVADLIPVIEKEY 9619

Query: 62 EFWIKNR 68 (SEQ ID NO:250)

FW + R (SEQ ID NO:251)

Sbjct: 9618 TFWSERR 9598 (SEQ ID NO:252)

Score = 182 (83.8 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95

Identities = 32/92 (34%), Positives = 55/92 (59%), Frame = -2

Query: 146 MDSIRTWSIIPADLNAFMCANARILASLYEIAGDFKKVKVFEQRYTWAKREMRELHWNENET 205
+ +I T +I+P DLNAF+C N I+ Y++ G+ K + R+T + ++ +
Sbjct: 9372 ISTIETTNIVPVDLNAFLCYNMNIMQLFYKLTGNPLKHLEWSSRFTNFREAFTKVIFYVPA 9193

Query: 206 DGIWYDYDIELKTHSNQYYVSNAPPLYAKCYD 237 (SEQ ID NO:253)

WYDY++ TH+ ++ SNAVPL+++CYD (SEQ ID NO:254)

Sbjct: 9192 RKGWYDYNLRTLTHNTDFFASNAVPLFSQCYD 9097 (SEQ ID NO:255)

Score = 178 (81.9 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95

Identities = 37/102 (36%), Positives = 55/102 (53%), Frame = -2

Query: 246 VHDYLERQGLLKYTEKGLPTSLAMSSTQQWDKENAWPPMIHVMIEGFRTTGDIKLMKVAEK 305
V++ ++ G G+PTS+ + QQWD N W PM HM+IEG R + + L + A
Sbjct: 9069 VYNEMQNSGAFSIPGGIPTSMNEETNQQWDFPNGWSPMNHMIIEGLRKSNNPILQQKAFT 8890

Query: 306 MATSWLTGTYQSFIRTHAMFEKYNVTPHTEETSGGGGGGEYEV 347 (SEQ ID NO:256)

+A WL Q+F + M+EKYNV + + GG E +V (SEQ ID NO:257)

Sbjct: 8889 LAEKWLETNMQTFNVSDMWEKYNVKEPLGKLATGGEYEVQV 8764 (SEQ ID NO:258)

Score = 169 (77.8 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95

Identities = 29/58 (50%), Positives = 41/58 (70%), Frame = -2

Query: 84 YQYKAKLKVPRPESYREDSELAEHLQTEAEKIQMWSEIASAAETGWDFSTRWFSQNGD 141

(SEQ ID NO:259)

+QY+ + + PRPES+RED AEH T+ K Q + + SAAE+GWDFS+RWF + D

(SEQ ID NO:260)

Sbjct: 9546 FQYRTEAETPRPESFREDVLSAEHFTTKDRKKQFFKDLGSAAESGWDFSSRWFKNHKD 9373

(SEQ ID NO:261)

Score = 76 (35.0 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95
Identities = 13/21 (61%), Positives = 15/21 (71%), Frame = -1

Query: 348 QTGFGWTNGVILDLLDKYGDQ 368 (SEQ ID NO:262)
Q GFGWTNG LDL+ Y D+ (SEQ ID NO:263)

Sbjct: 8722 QAGFGWTNGAALDLIFTYSR 8660 (SEQ ID NO:264)

Score = 45 (20.7 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95
Identities = 10/24 (41%), Positives = 15/24 (62%), Frame = -1

Query: 371 SSSTASKFSFSLSNITFVVFI LYI 394 (SEQ ID NO:265)
+SS++S F +S VF+LYI (SEQ ID NO:266)

Sbjct: 8545 TSSSSSTFGYSNLTITVFLYI 8474 (SEQ ID NO:267)

Score = 38 (17.5 bits), Expect = 2.6e-98, Sum P(7) = 2.6e-98
Identities = 7/7 (100%), Positives = 7/7 (100%), Frame = -2

Query: 342 GGEYEVQ 348 (SEQ ID NO:268)
GGEYEVQ (SEQ ID NO:269)

Sbjct: 8787 GGEYEVQ 8767 (SEQ ID NO:270)

Score = 37 (17.0 bits), Expect = 1.6e-19, Sum P(4) = 1.6e-19
Identities = 8/18 (44%), Positives = 10/18 (55%), Frame = -2

Query: 217 KTHSNQYYVSNAVPLYAK 234 (SEQ ID NO:271)
K ++ YYVS P Y K (SEQ ID NO:272)

Sbjct: 30345 KFTAHPYYVSRTPPRYHK 30292 (SEQ ID NO:273)

>W05E10

Length = 31,273
Minus Strand HSPs:

Score = 224 (103.1 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 43/67 (64%), Positives = 49/67 (73%), Frame = -1

Query: 2 VIKNLGYMVDNHGFVPNGGRVYYLTRSQPPLLTPMVYEEY MSTGDLD FVMEILPTLDKEY 61
+I+NL MVD +GFVPNGGRVYYL RSQPP L MVYE Y+ T D FV E+LPTL KE

Sbjct: 28957MIRNLASMVDKYGFVPNGGRVYYLQRSQPPFLAAMVYELYEATNDKAFVAELLPTLLKEL28778

Query: 62 EFWIKNR 68 (SEQ ID NO:274)
FW + R (SEQ ID NO:275)

Sbjct: 28777 NFWNEKR 28757 (SEQ ID NO:276)

Score = 192 (88.4 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 31/84 (36%), Positives = 52/84 (61%), Frame = -3

Query: 154 IIPADLNAFMCANARILASLYEIIAGDFKKVKVFEQRYTWAKREMRELHWNEDGIWYDYD 213
++P DLN + C N I + LYE GD K ++F + + ++ + +N TDG WYDY+
Sbjct: 2842 7VLPVDLNGLLCWNMDIMEYLYEQIGDTKNSQIFRNKRADFRDTVQNVFYNRTDGTWYDYN 28248

Query: 214 IELKTHSNQYYVSNAVPLYAKCYD 237 (SEQ ID NO:277)
+ ++H+ ++Y S AVPL+ CY+ (SEQ ID NO:278)
Sbjct: 28247 LRTQSHNPRFYTSTAVPLFTNCYN 28176 (SEQ ID NO:279)

Score = 125 (57.5 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 20/48 (41%), Positives = 30/48 (62%), Frame = -2

Query: 249 YLERQGLLKYTEKGLPTSLAMSSTQQWDKENAWPPMIHVMIEGFRTTGD 296 (SEQ ID NO:280)
+ ++ G+ Y G+PTS++ S QQWD N W P HM+IEG R + + (SEQ ID NO:281)
Sbjct: 28092 FFQKMGVFTYPPGGIPTSMSQESDQQWDFPNGWSPNNHMIIEGLRKSAN 27949 (SEQ ID NO:282)

Score = 90 (41.4 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 15/18 (83%), Positives = 18/18 (100%), Frame = -2

Query: 120 EIASAAETGWDFSTRWFS 137 (SEQ ID NO:283)
++ASAAE+GWDFSTRWFS (SEQ ID NO:284)
Sbjct: 28566 DLASAAESGWDFSTRWFS 28513 (SEQ ID NO:285)

Score = 89 (41.0 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 18/40 (45%), Positives = 24/40 (60%), Frame = -1

Query: 79 KQFPYYQYKAKLKVPRPESYREDSELAEHLQTEAEKIQMW 118 (SEQ ID NO:286)
K F YQYK VPRPESYR D++ + L A++ Q + (SEQ ID NO:287)
Sbjct: 28732 KSFKVYQYKTASNVP RPESYRVDTQNSAKLANGADQQQFY 28613 (SEQ ID NO:288)

Score = 77 (35.4 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 14/21 (66%), Positives = 16/21 (76%), Frame = -3

Query: 348 QTGFGWTNGVILDLLDKYGDQ 368 (SEQ ID NO:289)
Q GFGW+NG ILDLL Y D+ (SEQ ID NO:290)
Sbjct: 24395 QDGFWSNGAILDLLLTYNDR 24333 (SEQ ID NO:291)

Score = 51 (23.5 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 11/27 (40%), Positives = 16/27 (59%), Frame = -3

Query: 365 YGDQFASSSTASKFSFSLSNITFVVFI 391 (SEQ ID NO:292)
Y FASSS AS FS +++ F + + (SEQ ID NO:293)
Sbjct: 2846 YN*PFASSSDASSCPFSTNSVIFSILV 2766 (SEQ ID NO:294)

Score = 41 (18.9 bits), Expect = 3.3e-93, Sum P(8) = 3.3e-93
Identities = 7/9 (77%), Positives = 8/9 (88%), Frame = -2

Query: 340 GGGGEYEVQ 348 (SEQ ID NO:295)
G GGEY+VQ (SEQ ID NO:296)
Sbjct: 24468 GSGGEYDVQ 24442 (SEQ ID NO:297)

Score = 39 (18.0 bits), Expect = 2.0e-37, Sum P(5) = 2.0e-37
Identities = 7/14 (50%), Positives = 8/14 (57%), Frame = -2

Query: 221 NQYYVSNAVPLYAK 234 (SEQ ID NO:298)
N YY+ V LY K (SEQ ID NO:299)
Sbjct: 4524 NHYYIIQMVSPLYTK 4483 (SEQ ID NO:300)

Score = 38 (17.5 bits), Expect = 4.0e-88, Sum P(7) = 4.0e-88
Identities = 11/30 (36%), Positives = 13/30 (43%), Frame = -1

Query: 367 DQFASSSTASKFSFSLSNITFVVFILYIFS 396 (SEQ ID NO:301)
DQF S SKFS + F +FS (SEQ ID NO:302)
Sbjct: 7588 DQFVISFICKSFSSKNKKLYFCPSHFSLFS 7499 (SEQ ID NO:303)